

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/549,241
Source: PUS/10
Date Processed by STIC: 9/28/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/549,241

DATE: 09/28/2005

TIME: 13:45:54

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09282005\J549241.raw

3 <110> APPLICANT: Genentech, Inc.
 5 <120> TITLE OF INVENTION: COMPOSITIONS WITH HEMATOPOIETIC AND IMMUNE ACTIVITY
 7 <130> FILE REFERENCE: 11669.162WOU1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/549,241
 C--> 10 <141> CURRENT FILING DATE: 2005-09-12
 12 <150> PRIOR APPLICATION NUMBER: US 60/454,462
 13 <151> PRIOR FILING DATE: 2003-03-12
 15 <150> PRIOR APPLICATION NUMBER: US 60/511,390
 16 <151> PRIOR FILING DATE: 2003-10-14
 18 <160> NUMBER OF SEQ ID NOS: 40
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 427
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: cDNA encoding a human Bv8 homologue
 30 <400> SEQUENCE: 1

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33 gctgctgctc acgccccgacgc ctggggacgc cgccgtgatc accggggctt gtgacaaggaa	120
35 ctcccaatgt ggtggaggca tgtgctgtgc tgtcaagtatc tgggtcaaga gcataaggat	180
37 ttgcacacct atgggcaaac tgggagacag ctgcatcca ctgactcgta aaaacaattt	240
39 tggaaatgga aggcaggaaaa gaagaaaagag gaagagaagc aaaaggaaaa aggaggttcc	300
41 attttttggg cggaggatgc atcacacttg cccatgtctg ccaggcttgg cctgtttacg	360
43 gacttcattt aaccgattta tttgttagc ccaaaagtaa tcgctctgga gtagaaacca	420
45 aatgtga	427

48 <210> SEQ ID NO: 2
 49 <211> LENGTH: 129
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Homo sapiens
 53 <400> SEQUENCE: 2

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56 1 5 10 15	
59 Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr Gly	
60 20 25 30	
63 Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val	
64 35 40 45	
67 Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu	
68 50 55 60	
71 Gly Asp Ser Cys His Pro Leu Thr Arg Lys Asn Asn Phe Gly Asn Gly	
72 65 70 75 80	
75 Arg Gln Glu Arg Arg Lys Arg Lys Arg Ser Lys Arg Lys Lys Glu Val	
76 85 90 95	

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79 Pro Phe Phe Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly
 80 100 105 110
 83 Leu Ala Cys Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln
 84 115 120 125

87 Lys

91 <210> SEQ ID NO: 3

92 <211> LENGTH: 423

93 <212> TYPE: DNA

94 <213> ORGANISM: Artificial Sequence

96 <220> FEATURE:

97 <223> OTHER INFORMATION: cDNA encoding human Bv8 homologue

99 <400> SEQUENCE: 3

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102	gagggcgcca	tgaggagct	gtgctgcgc	ccactcctg	tcctcttgc	gctgccgccc	120
104	ctgctgctca	cgcgcgcgc	tggggacgcc	gccgtatca	ccggggcttg	tgacaaggac	180
106	tcccaatgtg	gtggaggcat	gtgctgtgt	gtcagtatct	gggtcaagag	cataaggatt	240
108	tgcacaccta	tgggcaaact	gggagacagc	tgcacatccac	tgactcgtaa	agttccattt	300
110	tttgggcgga	ggatgcatca	cacttgcaca	tgtctgccag	gcttggcttg	tttacggact	360
112	tcatttaacc	gattatttg	tttagccaa	aagtaatcgc	tctggagtag	aaaccaaatg	420
114	tga						423

117 <210> SEQ ID NO: 4

118 <211> LENGTH: 108

119 <212> TYPE: PRT

120 <213> ORGANISM: Homo sapiens

122 <400> SEQUENCE: 4

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128	Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr Gly						
129	20	25	30				
132	Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Met Cys Cys Ala Val						
133	35	40	45				
136	Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu						
137	50	55	60				
140	Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg						
141	65	70	75	80			
144	Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg						
145	85	90	95				
148	Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys						
149	100	105					

152 <210> SEQ ID NO: 5

153 <211> LENGTH: 1338

154 <212> TYPE: DNA

155 <213> ORGANISM: Mus musculus

157 <400> SEQUENCE: 5

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160	ctgtgccccg	ctactgctac	ttctgctgt	accgctgctg	ttcacacccgc	ccggccgggga	120
162	tgccgcggtc	atcaccgggg	cttgcgacaa	ggactctcag	tgcggagag	gcatgtgctg	180
164	tgctgtcagt	atctgggta	agagcataag	gatctgcaca	cctatgggcc	aagtgggcga	240
166	cagctgccac	cccctgactc	ggaaaattcc	attttggggg	cgaggatgc	accacacctg	300

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168	ccccgtgcctg	ccaggcgttgg	cgtgttaag	gacttcttc	aaccgggtta	tttgcttggc	360												
170	ccggaaatga	tcactctgaa	gttaggaacct	gaaatgcgac	cctccgctgc	acaatgtccg	420												
172	tgcgtctca	cttgcatttg	tggcaaacaa	agaataactcc	agaaagaaat	gttctccccc	480												
174	tcccttgact	ttccaagtaa	cgtttctatac	tttgcatttt	gaagtggctt	tttttttttt	540												
176	tttttttcc	tttccttggaa	ggaaagttt	gatttttggaa	gagatttata	gaggactttc	600												
178	tgacatggct	tctcatttcc	ctgtttatgt	tttgccttga	catttttggaa	tgccaataaac	660												
180	aactgttttcc	acaaatagga	gaataagagg	gaacaatctg	ttgcagaaaac	ttccttttgc	720												
182	cctttggccc	actcgccccg	ccccggcccc	ccccggccctg	cccatgcgca	gacagacaca	780												
184	cccttactct	tcaaagactc	tgatgatcct	caccttactg	tagcatttg	ggtttctaca	840												
186	cttcccccgc	ttgctggtgg	acccactgag	gaggctcaga	gagctagcac	tgtacagggtt	900												
188	tgaaccagat	cccccaagca	gctcattttgg	ggcagacgtt	gggagcgctc	caggaacttt	960												
190	cctgcaccca	tctggcccac	ttggcttcag	ttctgcgttt	taactggtgg	gaggacaaaa	1020												
192	ttaacgggac	cctgaaggaa	cctggccctgt	ttatctagat	ttgtttaagt	aaaagacatt	1080												
194	ttctccttgc	tgtggatat	tacatgtctt	tttctttttt	atctgaagct	tttttttttt	1140												
196	ttctttaagt	tttctgttg	gagacatttt	aaagaacgcc	actcgagaa	gcattgattt	1200												
198	tcatytggca	tgacaggagt	catcattttt	aaaaatcggt	gttaagtat	aattttaact	1260												
200	ttatttgtaa	cccaaaggty	taatgtaaat	ggatttcctg	atatcgtcc	atttgtactg	1320												
202	gtatcaatat	ttytatgt					1338												
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216	Leu	Leu	Phe	Thr	Pro	Pro	Ala	Gly	Asp	Ala	Ala	Val	Ile	Thr	Gly	Ala			
217							20			25				30					
220	Cys	Asp	Lys	Asp	Ser	Gln	Cys	Gly	Gly	Gly	Met	Cys	Cys	Ala	Val	Ser			
221							35			40				45					
224	Ile	Trp	Val	Lys	Ser	Ile	Arg	Ile	Cys	Thr	Pro	Met	Gly	Gln	Val	Gly			
225							50			55				60					
228	Asp	Ser	Cys	His	Pro	Leu	Thr	Arg	Lys	Val	Pro	Phe	Trp	Gly	Arg	Arg			
229							65			70				75				80	
232	Met	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Gly	Leu	Ala	Cys	Leu	Arg	Thr			
233							85			90				95					
236	Ser	Phe	Asn	Arg	Phe	Ile	Cys	Leu	Ala	Arg	Lys								
237							100			105									
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245	<220>	FEATURE:																	
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251	ggcagtgttt	tgccttcacc	ccaagtgacc	atgagagggt	ccacgcgagt	ctcaatcatg												120	
253	ctcctcctag	taactgtgtc	tgactgtgtc	gtgatcacag	gggcctgtga	gcgggatgtc												180	
255	cagtgtgggg	caggcacctg	ctgtgccatc	agcctgtggc	ttcgagggt	gcggatgtc												240	
257	accccgctgg	ggcgaaaagg	cgaggagtgc	caccccgcc	gccacaagg	cccttcttc												300	

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259	aggaaaacgca	agcaccacac	ctgtccttgc	ttgcccaacc	tgctgtgctc	caggttcccc	360										
261	gacggcgagg	accgctgctc	catggacttg	aagaacatca	atttttaggc	gcttcctgg	420										
263	tctcaggata	cccaccatcc	tttccttag	cacagcctgg	atttttattt	ctggcatgaa	480										
265	acccagctcc	catgactctc	ccagtccta	cactgactac	cctgatctt	cttgtctagt	540										
267	acgcacatata	gcacacaggc	agacataacct	cccatcatga	catggtcccc	aggctggcct	600										
269	gaggatgtca	cagcttgagg	ctgtgggtgt	aaaggtggcc	agcctgggtc	tctccctgc	660										
271	tcaggctgcc	agagaggtgg	taaatggcag	aaaggacatt	ccccctcccc	tccccaggtg	720										
273	acctgctctc	tttcctggc	cctgcccctc	tccccacatg	tatccctcg	tctgaattag	780										
275	acattcctgg	gcacaggctc	ttgggtgcat	tgctcagagt	cccaggctct	ggcctgacccc	840										
277	tcaaggccctt	cacgtgaggt	ctgtgaggac	caatttgtgg	gtagttcatc	ttccctcgat	900										
279	tgttaactc	tttagttca	gaccacagac	tcaagattgg	ctcttccag	aggcagcag	960										
281	acagtccacc	caaggcagg	gtagggagcc	cagggaggcc	aatcagcccc	ctgaagactc	1020										
283	tggtcccagt	cagcctgtgg	cttgcgtgc	gtgacctgt	accttctgcc	agaattgtca	1080										
285	tgcctctgag	gccccctctt	accacactt	accagttaac	caactgaagcc	cccaattcccc	1140										
287	acagctttc	cattaaaatg	caaatggtg	tggtcaatc	taatctgata	ttgacatatt	1200										
289	agaaggcaat	tagggtgtt	ccttaaaca	ctccttcca	aggatcagcc	ctgagagcag	1260										
291	gttggtgact	ttgaggaggg	cagtccctg	tccagattgg	ggtgggagca	aggacaggg	1320										
293	agcagggcag	gggctgaaaag	gggcactgat	tcagaccagg	gaggcaacta	cacaccaaca	1380										
295	tgctggctt	agaataaaag	caccaactga	aaaaaa			1415										
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309	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val	Gln	Cys	
310					20					25					30		
313	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg	Gly	Leu	Arg	
314					35					40					45		
317	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser	
318					50					55					60		
321	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys	
322	65				70					75					80		
325	Leu	Pro	Asn	Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	
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344	ctgtgcata	tttcatcatg	ctccttctag	caacggcg	cgactgtgcg	gtcatcacag	120										
346	gggcctgtga	acgagatatac	cagtgggg	ccggcacctg	ctgcgtatc	agtctgtggc	180										
348	tgcggggcct	gcgggtgtgt	accccactgg	ggcgtgaagg	agaggagtgc	cacccaggaa	240										

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354	tttagtttgt	ctggactctg	tctggagctt	gactgggtga	cctcttgctt	tacacctgtg	420										
356	tgathtagct	ccctgcaact	tcgccattcc	ccatcttgc	cgtgtatgt	cagacaggca	480										
358	gacccttccgc	tatggaatag	ttcaccaggg	tgcagagagg	agttcggtgc	cttggagaagt	540										
360	tggccagccc	gaccttcctg	gctcagactg	cctgaagttt	tgacagtgt	ggccttctca	600										
362	gttgcctgcc	ccttcctgca	tgtgcgttc	ttccctaaacc	acaccttct	ggcactggc	660										
364	ccatggatgc	accactaaat	caacaggctt	gtgggggtgga	tgtcaactt	tctccatt	720										
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370	<211>	LENGTH:	105														
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380	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Ile	Gln	Cys	
381					20					25					30		
384	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg	Gly	Leu	Arg	
385					35					40					45		
388	Leu	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser	
389					50					55					60		
392	His	Lys	Ile	Pro	Phe	Leu	Arg	Lys	Arg	Gln	His	His	Thr	Cys	Pro	Cys	
393					65					70					75		80
396	Ser	Pro	Ser	Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date